

Figure 1A

1	CAAGCACTGTGCTAAAGTGTTCATATGTCATGAAAAGTTGTGCCAGAAAATTATGGT	60
61	TTGAACATGGGCAGTTCTCCTACCGTCAGCTATATCCACAAGCATCACATGAAGTGGA	120
121	GACTGGCAGCTCTGTGTATTCAGTCAAGTCCACAATGAAACCTGACAATAATGGTAA	180
181	AAACCAATACGGACATCTGAGTAACGGGAATTGGCCTGCATGTGAGCTTGATG	240
241	GAAGATTGGATATAGACCGAGTTGATTATATTTATGAAGTAGCAGCTCACTACCAC	300
301	CATCCAGGGTTAAACTACTTTTCAGCATCACTCACCTGTGGACTCTTACACATTG	360
361	ATTCTTGGGGAAAAACTGGGATAAGAGGAGGTCACTTTAATAAGTTAGCATTCT	420
421	TTTCCCTTCTTACAAGTTGATCAAAGGATAAGGCTGTGACTCCATTGGATTGCACCTT	480
481	TAAATCAAAATAGCAGCAGCAGAAGAAAGGGACAATGGCTCTGAGTGGAAACTGTAGTCG	540
1	M A L S G N C S R	9
541	TTATTATCCTCGAGAACAAAGGGTCCGCAGTTCCAACTCCTCCCTGAGGTGGTAGAGCT	600
10	Y Y P R E Q G S A V P N S F P <u>E</u> V V E L	29
601	GAATGTCGGGGTCAAGTTATTTACTCGCCATTCCACATTGATAAGCATCCCTCATTC	660
30	<u>N V G G Q V Y F T R H S T L I S I P H S</u>	49
661	CCTCCTGTGGAAATGTTCCCAAAGAGAGACACGGCTAATGATCTAGCCAAGGACTC	720
50	<u>L L W K M F S P K R D T A N D L A K D S</u>	69
721	CAAGGGAAAGGTTTCTTGCACAGAGATGGATTCTGTTCCGTTATATTCTGGACTATCT	780
70	<u>K G R F F I D R D G F L F R Y I L D Y L</u>	89
781	CAGGGACAGGCAGGTGGCCTGCCTGATCACTTCCAGAAAAGGAAGACTGAAAAGGGA	840
90	<u>R D R Q V V L P D H F P E K G R L K R E</u>	109
841	AGCTGAATACTCCAGCTCCAGACTGGTCAAACCTCCTGACCCCCGATGAAATCAAGCA	900
110	<u>A E Y F Q L P D L V K L L T P D E I K Q</u>	129
901	AAGCCCAGATGAATTCTGCCACAGTGACTTTGAAGATGCCCTCCAAAGGAAGCGACACAAG	960
130	<u>S P D E F C H S D F E D A S Q G S D T R</u>	149
961	AATCTGCCCTTCCCTGCTCCCTGCCGACCGCAAGTGGGTTTCATTACTGTGGG	1020
150	<u>I C P P S S L L P A D R K W G F I T V G</u>	169

Figure 1B

1021	TTACAGAGGATCCTGCACCTGGCAGAGAGGGACAGGCAGATGCCAAGTTGGAGAGT	1080
170	Y R G S C T L G R E G Q A D A K F R R V	189
1081	TCCCCGGATTTGGTTGTGAAGGATTCTCTGGAAAAGAAGTCTTGAGAAACTT	1140
190	P R I L V C G R I S L A K E V F G E T L	209
1141	GAATGAAAGCAGAGACCTGATCGAGCCCCAGAAAGATAACCTCCAGATTTATCTCAA	1200
210	N E S R D P D R A P E R Y T S R F Y L K	229
1201	ATTCAAGCACCTGGAAAGGGCTTTGATATGTTGTCAGAGTGTGGATTCCACATGGTGGC	1260
230	F K H L E R A F D M L S E <u>C G F H M V A</u>	249
1261	CTGTAACTCATCGGTGACAGCATCTTCATCAACCAATATACAGATGACAAGATCTGGTC	1320
250	<u>C N S S V T A S F I N Q Y T D D K I W S</u>	269
1321	AAGCTACACTGAATATGTCCTCTACCGTGAGCCTTCCAGATGGTCACCCCTCACACTGCGA	1380
270	S Y T E Y V F Y R E P S R W S P S H C D	289
1381	TTGCTGCTGCAAGAATGCCAAAGGTGACAAAGAAGGGAGAGCGGCACGTCTTGCAATGA	1440
290	C C C K N G K G D K E G E S G T S C N D	309
1441	CCTCTCCACATCTAGCTGCGACAGCCAGTCTGAGGCCAGCTCTCCCAGGAGACGGTCAT	1500
310	L S T S S C D S Q S E A S S P Q E T V I	329
1501	CTGTGGTCCCGTGACACGCCAGACCAACATCCAGACTCTGGACCGTCCATCAAGAAGGG	1560
330	C G P V T R Q T N I Q T L D R P I K K G	349
1561	CCCTGTCCAGCTGATCCAACAGTCAGAGATGCCGGAAAAGCGACTTACTCCGGATTCT	1620
350	P V Q L I Q Q S E M R R K S D L L R I L	369
1621	GACTTCAGGCTCCAGGGATCGAACATGAGCAGCAAAAAAAAGCTGTTAAAGAAAAGCT	1680
370	T S G S R E S N M S S K K K A V K E K L	389
1681	CTCAATTGAGGAGGAGCTGGAGAAATGTATCCAGGATTCCTAAAAAAATTCCAGA	1740
390	S I E E L E K C I Q D F L K K K I P D	409
1741	TCGGTTCTGAGAGAAAACATCCTGGCAATCTGAACTTAAAGGAAGTATCATCTATA	1800
410	R F P E R K H P W Q S E L L R K Y H L	428
1801	AGGGAGGGCTGGGGCGGGAAAAAAAGAGTCATTTGAAATTACCTCATAA	1860
1861	AAGGAATTCATATTTAAAGGAAAAAAATACAACTAATGATGCACATTCTTAGAACACA	1920
1921	ATAGTCCATTGATATACTACTGCCTACTTACCTAGTTCACCTAACATGTAAATCCACA	1980

**Figure 1C**

1981	GGGTAGATTCTTCTAGATGTGGAAGTACAAGAAAATCTTTTAGTTATTGTTGTT	2040
2041	TACTTCGTCCCAGTGCTAACTATCTTATATAATGAGAGCCAGCTACGTAAAAGTAGC	2100
2101	TGAGAGGCCCTGGGAGTCATTTATCCAAACTGGGTTTTCTCATCCTCTACCTCC	2160
2161	CTCCTTGAAATGAGGGTATGGTAGAAAAAGATCTGGCCCAATGGCATAAGTTGGAATT	2220
2221	TTAATTTGGTTTTCCCTTGTGTTATGGGTTGGGGGAATGGCAGATTATATGACTT	2280
2281	TTCACTCAAATCTATATGTGCCAGTTATATTGACTCCGTATGCATGAGTATTGTGCAA	2340
2341	CACAAGCACAACTAAGTATGTATATACACATGACGCACACGATGCCAGGGCTAGACCTC	2400
2401	CCAAGGGCTGTGCTCCTGCTCCCAGCAGCCCTCTTAGAATATTCAGATGGATGAGCT	2460
2461	TCTGACTCTTCTTAAATTCTTGGGAAGATTCCCAGCCTTCTTCACAACACTTTC	2520
2521	TAACATCAAATGACTCTCATCAACAAATTGTATTCTTATTGTGAAATTAAATACCCCT	2580
2581	CAGGCTCCATTTACTGCTTGCTTGTCTGCATTAAGAGAGGATGAGGAGAGCTGGT	2640
2641	CAAACATTCTGTGTTAAAAAAATCAAACATTCAATCCACAAATTCTGCTAAATG	2700
2701	ACTCCACACTCAGCCTCTCACCTGAACCTGAATTATCACCCCTTCTCCATGTTTCA	2760
2761	GAGTTCTTACTGCCACAGTTAATGGTGTGGCCTTCACATAATCCACATTAAGTTCT	2820
2821	GTGTTCTGTGTTGTGGAACTAAGGACAACACACAGTACTTGAATAAGGGTCCGGCC	2880
2881	TTTGTTGTTAGAGAAAGTTGTATTCCACACACAACCTAATAATTCTTATAAAAAT	2940
2941	TTTAAACTACAAAGCTACATTCTACTTGCTGTAGCCGTTTGTGCTTGGGATT	3000
3001	CGGGCTTGCGCTGTGCCAGCTAGGATTAGCTGTGTCATTATGATGTCTGTAACA	3060
3061	ACCCAACAAGGTAACGTAAAGCTCCAGAGTTAAGGTTCAAGATTCTAAATGAAACTATCT	3120
3121	TTTCAATTACATCCTGACTGTATAGACACAGCCAAAAAGAAACTGTTAATAGCCATCC	3180

D0076 NP

Figure 1D

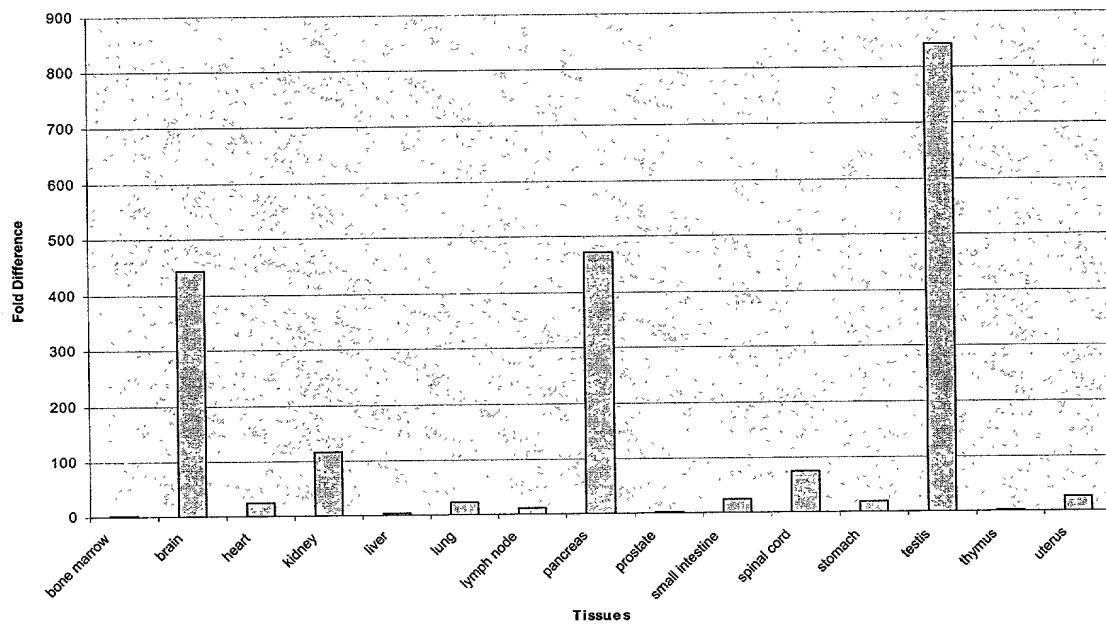
Figure 2A

		50
K+betaM2	(1) -----MALSGNCSRYYPREQSAVPNSH	PEVELNVGGQYFTRHSTLIS
AAF558201	(1) -----	MPTEELNVGGVSYTTLATLLO
CAA20329.1	(1) -----	MTSVEDEVTLNVGGBTYTTTGSTLSK
Y34129	(1) -----	MDNGDWGYMMTDPTVLNVGGHLYTTSILTLTR
Y34125	(1) MSRPLITRSPASPLXNQGIPTPAQLTKSNAPVH	VGHHMYTSSLATLTK
	51	100
K+betaM2	(46) IPSLLWKMFSP--KRDTAND	AKDSKGRRFIDRDGFIFRYILDMLRDRQ
AAF558201	(24) DKSTLLAELFG-----	GRDSIAKDSKGRYFIDRDGVLFYILDFLRDKA
CAA20329.1	(27) ETPLLANTASGSLSEDEQANV	TLPPGTLFIDRDGPLFAYLHFRLRTDK
Y34129	(33) YPSMILGAMFGG---D--	FPTARDPQGNYFIDRDGPLFAYLNFRLRTSE
Y34125	(51) YPESRGRIFDG---T-EPIVLD	SLKQHYFIDRDGQMFRYILNFRLRTSK
	101	150
K+betaM2	(94) VLPDPHFPEKGR	LKREADYFQLPDWKLTPDIIKQSPDEFCHSDFEDAS
AAF558201	(69) LHLPEGFRERQRILLR	AEAHFKLTAMIECIRSEEDAR-----
CAA20329.1	(77) LSLPQEQRREV	ARLKDEADPHYRLERFSTLLSNASSIS-PRPR-----
Y34129	(77) LTLPLDFKEFDLLR	KREADPQIEPLIQCLNDPFLPLY-----
Y34125	(96) LL	LPDFKDYTLLYBEAKFQLQPMILEMERWQDQR-----
	151	200
K+betaM2	(144) QGSDTRICPPSSLLPADRKWGFIT	GYRGSCTLREGQADAKFRRVPRL
AAF558201	(105) -----PP---GCIT	GYRGSFQFGKDGGLADVKFRKLSRIL
CAA20329.1	(117) -----TANGYNTIT	SGAETGGYITLGYRGTFAFGRDUGQADVKFRKLIHRIL
Y34129	(113) -----PMDFEEV	VELSTRKLSKYSNPVAVITOLIITTK
Y34125	(132) -----ETGRFSRPCECLVVRVAPDLGERITL	SGDKSLIEEVL
	201	250
K+betaM2	(194) VCGRTISLAKEVFG	FTLNESRDPDR-APERYTSRFYLFKHLERAFLDMLSE
AAF558201	(137) VCGRVAQC	REVFGDTLNESRDPDHGGTDRYTSRFFLKHCVIEQAFDNLHD
CAA20329.1	(162) VCGRATIC	CREVFAITLNESRDPGG-PDGF-----
Y34129	(149) VHSL	EGISNYFTKWNKIMMDPDRD-CQVSTFTGPCDYQEVSRLVHLM
Y34125	(169) PEIGDVMCN	SVNAGWNHDSTHVIR-FPLNGYCHLNSVQVLERLQQ
	251	300
K+betaM2	(243) CGTHMVP	CNSSVTASFIN-----QYTD
AAF558201	(187) HGYR	MAKGSCSGTAGSAAEPKPGVDTEENRWNHYNEFVFIRD
CAA20329.1	(191) -----	-----
Y34129	(196) EY	TKQGFTIRNTRVHHMSERANENTVHNWTFCRLLARKTDD
Y34125	(213) RG	FEVGSCGGGDSSQFSEYVLRELRTPRVPSVIRIKQPL
	301	350
K+betaM2	(288) CCCCCKNGKGDKEGESGT	CNDLSTSSCDSQSEASSPQETVICGPVTRQT
AAF558201	(229) -----	
CAA20329.1	(191) -----	
Y34129	(238) -----	
Y34125	(257) -----	
	351	400
K+betaM2	(338) NIQTLDRPIKKGPVQLIQQSEMRKSDLLRIL	TSGSRESNMSSKKKAVKE
AAF558201	(229) -----	
CAA20329.1	(191) -----	
Y34129	(238) -----	
Y34125	(257) -----	

**Figure 2B**

	401	441
K+betaM2	(388) KLSIEEELEKCIQDFLKKKIPDRFPERKHPWQSELLRKYHL	
AAF558201	(229) -----	-----
CAA20329.1	(191) -----	-----
Y34129	(238) -----	-----
Y34125	(257) -----	-----
Consensus	(401)	

Figure 3



**Figure 4.**

Protein	Genbank ID	Identities	Similarities
Human potassium channel K+Hnov28	gi Y34129	31%	41%
Drosophila CG10830 protein	gi AAF55820.1	52%	66%
Caenorhabditis K+ channel tetramerisation domain	gi CAA20329.1	42%	51%
Human potassium channel K+Hnov27	gi Y34125	32%	41%

Figure 5

